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NOV 29 2001

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SEQUENCE LISTING

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MANCUSO, DAVID J.

<120> CALCIUM INDEPENDENT PHOSPHOILPASE A2Y POLYNUCLEOTIDES
AND POLYPEPTIDES AND METHODS THEREFOR

<130> 15060-0004

<140> 09/618,623

<141> 2000-07-18

<160> 47

<170> PatentIn Ver. 2.1

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<212> PRT

<213> Homo sapiens

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Gly Phe His Thr Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala
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His Ser Cys Ser Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His
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Ile Gly Ile Leu Lys Leu Ser Thr Ser Ala Pro Lys Gly Leu Thr Lys
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Val Asn Ile Cys Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser
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Glu	Ser	Arg	Asn	Glu	Lys	Leu	Asp	Gln	Leu	Gln	Leu	Glu	Gly	Leu	Lys	725	730	735
Tyr	Ile	Glu	Arg	Asn	Glu	Gln	Lys	Met	Lys	Lys	Val	Ala	Lys	Ile	Leu	740	745	750
Ser	Gln	Glu	Lys	Thr	Thr	Leu	Gln	Lys	Ile	Asn	Asp	Trp	Ile	Lys	Leu	755	760	765
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 Phe Ser Pro Lys His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg
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 Gly Phe His Thr Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala
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 Phe Lys Pro Ser Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp
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 Ser Asp Lys Ser Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His
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 Ile Ile Asp Lys Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr
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Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu	
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cat caa gat gga ggt ttg ctt ctg aat aac cct tcg gca tta gct atg	1920
His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met	
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Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp	
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Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu	
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Met Ser Ile Asn

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His Tyr Trp Arg Ile Ser His Ile Ser Leu Gln Arg Gly Phe His Thr
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Asn Ile Ile Arg Cys Lys Trp Thr Lys Ser Glu Ala His Ser Cys Ser
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Lys His Cys Tyr Ser Pro Ser Asn His Gly Leu His Ile Gly Ile Leu
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Val	Ser	Ile	Asp	Asn	Arg	Thr	Arg	Ala	Leu	Val	Gln	Ala	Leu	Arg	Arg	
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565 570 575 580	
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Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly	
585 590 595	
tgt cag tat aaa atg tgg cag gcc att aga gcc tca tct gct gct cca	2061
Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro	
600 605 610	
ggc tac ttt gca gaa tat gca ttg gga aat gat ctt cat caa gat gga	2109
Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly	
615 620 625	
ggg ttg ctt ctg aat aac cct tcg gca tta gct atg cat gag tgt aaa	2157
Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys	
630 635 640	

tgt ctt tgg cca gat gtg ccg tta gag tgc ata gta tcc ctg ggc act	2205
Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr	
645 650 655 660	
gga cgt tat gag agt gat gtg aga aac acg gta aca tac aca agc ttg	2253
Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu	
665 670 675	
aaa act aaa ctt tct aat gtt atc aac agt gct aca gat aca gaa gaa	2301
Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu	
680 685 690	
gtc cat ata atg ctt gat ggc ctg tta cct cct gac acc tat ttt aga	2349
Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg	
695 700 705	
ttc aat cct gta atg tgt gaa aac ata cct cta gat gaa agt cga aat	2397
Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn	
710 715 720	
gaa aag ctg gat cag ctg cag ttg gaa ggg ttg aaa tac ata gaa aga	2445
Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg	
725 730 735 740	
aat gaa caa aaa atg aaa aaa gtt gca aaa ata tta agt caa gaa aaa	2493
Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys	
745 750 755	
aca act ctg cag aaa att aat gat tgg ata aaa tta aaa act gat atg	2541
Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met	
760 765 770	
tat gaa gga ctt cca ttc ttt tca aaa ttg tgatgagtat atgcttatgt	2591
Tyr Glu Gly Leu Pro Phe Ser Lys Leu	
775 780	
tctcataaat gaaggtctgt ttagaagatc aaccacattc aataaggaat tgtgggggttc	2651
gacatgagtt aactttgaaa tacgtatgaa ttctggagaa tcctgaaaaa gacggtgctt	2711
caaccagctt gcatagcaca gagaatattc ttggttacag aattcatatg ggaactaggc	2771
ttttaagatg ttaataatta gctaagcttt agtaaccctt actgtgctag tagattttag	2831
tagatatggg tgttatatgg tttgatgttt gaaaatatat taatatatgt gccgaacaag	2891
aaaccgaaag ctatatgtga ctgtgtatgt ttactttagt cctcataatc atgttgaatt	2951
tatgtgatca ttgattttat ttcatatgga aaagctaatt tcttcttaaa ttacattac	3011
ctaataattct cactagctat gttctccaat ccacactgcc ttttattgta atatcatcta	3071
aatagatgca gaaaaatgga attttctcta ttaaagtatt ttacatttga cataaaaaag	3131
aaccagatac agttttctat tcagatatgt ttattttaac attgtttggg taaaaaagg	3191
gaagttccag tcaaccactt tttaccctg aaatttcaag ataatgctat attaaacttt	3251

<400> 5															
Met	Ser	Ile	Asn	Leu	Thr	Val	Asp	Ile	Tyr	Ile	Tyr	Leu	Leu	Ser	Asn
1				5					10					15	
Ala	Arg	Ser	Val	Cys	Gly	Lys	Gln	Arg	Ser	Lys	Gln	Leu	Tyr	Phe	Leu
			20					25					30		
Phe	Ser	Pro	Lys	His	Tyr	Trp	Arg	Ile	Ser	His	Ile	Ser	Leu	Gln	Arg
		35					40					45			
Gly	Phe	His	Thr	Asn	Ile	Ile	Arg	Cys	Lys	Trp	Thr	Lys	Ser	Glu	Ala
	50					55					60				
His	Ser	Cys	Ser	Lys	His	Cys	Tyr	Ser	Pro	Ser	Asn	His	Gly	Leu	His
65					70					75					80
Ile	Gly	Ile	Leu	Lys	Leu	Ser	Thr	Ser	Ala	Pro	Lys	Gly	Leu	Thr	Lys
				85					90					95	
Val	Asn	Ile	Cys	Met	Ser	Arg	Ile	Lys	Ser	Thr	Leu	Asn	Ser	Val	Ser
			100					105					110		
Lys	Ala	Val	Phe	Gly	Asn	Gln	Asn	Glu	Met	Ile	Ser	Arg	Leu	Ala	Gln
		115					120					125			
Phe	Lys	Pro	Ser	Ser	Gln	Ile	Leu	Arg	Lys	Val	Ser	Asp	Ser	Gly	Trp
	130					135					140				
Leu	Lys	Gln	Lys	Asn	Ile	Lys	Gln	Ala	Ile	Lys	Ser	Leu	Lys	Lys	Tyr
145				150						155					160
Ser	Asp	Lys	Ser	Ala	Glu	Lys	Ser	Pro	Phe	Pro	Glu	Glu	Lys	Ser	His
				165					170					175	
Ile	Ile	Asp	Lys	Glu	Glu	Asp	Ile	Gly	Lys	Arg	Ser	Leu	Phe	His	Tyr
			180					185					190		
Thr	Ser	Ser	Ile	Thr	Thr	Lys	Phe	Gly	Asp	Ser	Phe	Tyr	Phe	Leu	Ser
		195					200					205			
Asn	His	Ile	Asn	Ser	Tyr	Phe	Lys	Arg	Lys	Glu	Lys	Met	Ser	Gln	Gln
	210					215					220				
Lys	Glu	Asn	Glu	His	Phe	Arg	Asp	Lys	Ser	Glu	Leu	Glu	Asp	Lys	Lys
225				230						235					240

Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr
 245 250 255
 Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro
 260 265 270
 Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala
 275 280 285
 Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly
 290 295 300
 Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln
 305 310 315 320
 Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys
 325 330 335
 Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys
 340 345 350
 Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln
 355 360 365
 Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu
 370 375 380
 Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala
 385 390 395 400
 Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys
 405 410 415
 Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly
 420 425 430
 Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp
 435 440 445
 Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu
 450 455 460
 Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys
 465 470 475 480
 Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His
 485 490 495
 Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp
 500 505 510
 Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser
 515 520 525
 His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg
 530 535 540

Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro
 545 550 555 560
 Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys
 565 570 575
 Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His
 580 585 590
 Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser
 595 600 605
 Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu
 610 615 620
 His Gln Asp Gly Gly Leu Leu Asn Asn Pro Ser Ala Leu Ala Met
 625 630 635 640
 His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val
 645 650 655
 Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr
 660 665 670
 Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr
 675 680 685
 Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp
 690 695 700
 Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp
 705 710 715 720
 Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys
 725 730 735
 Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu
 740 745 750
 Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu
 755 760 765
 Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe Ser Lys Leu
 770 775 780

<210> 6

<211> 320

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (226)..(320)

<400> 6

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gccgctgcag ccctagtgac tgcggcctgc atcccgattg tcttctctc caaggtctac 120

atgattacct gaagtttaat aagtaagacc atgaattatg gcatttctta aatgaagcgt 180

tcaagaagtg agagaatgtc atagaaaata aatgattttt aagtt atg tct att aat 237
Met Ser Ile Asn

1

ctg act gta gat ata tat att tac ctc ctt agt aat gca aga agt gtt 285
Leu Thr Val Asp Ile Tyr Ile Tyr Leu Leu Ser Asn Ala Arg Ser Val
5 10 15 20

tgt ggg aag cag aga agc aag caa ctg tat ttc tt 320
Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu
25 30

<210> 7

<211> 274

<212> DNA

<213> Homo sapiens

<220>

<221> modified_base

<222> (121)

<223> a, t, c, g, other or unknown

<220>

<221> modified_base

<222> (158)

<223> a, t, c, g, other or unknown

<400> 7

tggaagctca gctgatgcag gccgggttga gtggacttca ttgccgggaa cgagcgagtc 60
gccgctgcag ccctagtgac tgcggcctgc atcccggtta gaccatgaat tatggcattt 120
nttaaatgaa gcgttcaaga agtgagagaa tgtcatanaa aataaatgat ttttaagtta 180
tgtctattaa tctgactgta gatatatata tttacctcct tagtaatgca agaagtgttt 240
gtgggaagca gagaagcaag caactgtatt tctt 274

<210> 8

<211> 193

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (15) .. (193)

<400> 8

tggaagctca gctg atg cag gcc ggt tgg agt gga cgt cat tgc cgg gaa 50
Met Gln Ala Gly Trp Ser Gly Arg His Cys Arg Glu
1 5 10

cga gcg agt cgc cgc tgc agc cct agt gac tgc ggc ctg cat ccc gat 98
Arg Ala Ser Arg Arg Cys Ser Pro Ser Asp Cys Gly Leu His Pro Asp
15 20 25

tgt ctt ctc ctc caa ggt cta cat gat tac ctg aag ttt aat aat aat 146
 Cys Leu Leu Leu Gln Gly Leu His Asp Tyr Leu Lys Phe Asn Asn Asn
 30 35 40

gca aga agt gtt tgt ggg aag cag aga agc aag caa ctg tat ttc tt 193
 Ala Arg Ser Val Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu
 45 50 55 60

<210> 9
 <211> 60
 <212> PRT
 <213> Homo sapiens

<400> 9
 Met Gln Ala Gly Trp Ser Gly Arg His Cys Arg Glu Arg Ala Ser Arg
 1 5 10 15
 Arg Cys Ser Pro Ser Asp Cys Gly Leu His Pro Asp Cys Leu Leu Leu
 20 25 30
 Gln Gly Leu His Asp Tyr Leu Lys Phe Asn Asn Asn Ala Arg Ser Val
 35 40 45
 Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu
 50 55 60

<210> 10
 <211> 32
 <212> PRT
 <213> Homo sapiens

<400> 10
 Met Ser Ile Asn Leu Thr Val Asp Ile Tyr Ile Tyr Leu Leu Ser Asn
 1 5 10 15
 Ala Arg Ser Val Cys Gly Lys Gln Arg Ser Lys Gln Leu Tyr Phe Leu
 20 25 30

<210> 11
 <211> 35
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

<400> 11
 tttgtcgcac atgtctatta atctgactgt agata 35

<210> 12
 <211> 38
 <212> DNA
 <213> Artificial Sequence

Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys Asp Arg Asn Ala
225 230 235 240

Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg
 245 250 255
 Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg
 260 265 270
 Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe
 275 280 285
 His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg
 290 295 300
 Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu
 305 310 315 320
 Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro
 325 330 335
 Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr
 340 345 350
 Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr
 355 360 365
 Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr
 370 375 380
 Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His Met Pro Leu Asp
 385 390 395 400
 Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln
 405 410 415
 Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr
 420 425 430
 Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala
 435 440 445
 Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala
 450 455 460
 Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe
 465 470 475 480
 Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly
 485 490 495
 Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro
 500 505 510
 Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly
 515 520 525
 Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys
 530 535 540

Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr
 545 550 555 560
 Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu
 565 570 575
 Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu
 580 585 590
 Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg
 595 600 605
 Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn
 610 615 620
 Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg
 625 630 635 640
 Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys
 645 650 655
 Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met
 660 665 670
 Tyr Glu Gly Leu Pro Phe Phe Ser Lys Leu
 675 680

<210> 14
 <211> 2049
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(2049)

<400> 14
 atg tcc cgt att aaa agt act ttg aac tct gtt tca aag gct gtt ttt 48
 Met Ser Arg Ile Lys Ser Thr Leu Asn Ser Val Ser Lys Ala Val Phe
 1 5 10 15
 ggc aat caa aat gaa atg att tca cgt tta gct caa ttt aag cca agt 96
 Gly Asn Gln Asn Glu Met Ile Ser Arg Leu Ala Gln Phe Lys Pro Ser
 20 25 30
 tcc caa att tta aga aaa gta tcg gat agt ggc tgg tta aaa cag aaa 144
 Ser Gln Ile Leu Arg Lys Val Ser Asp Ser Gly Trp Leu Lys Gln Lys
 35 40 45
 aac atc aaa caa gcc atc aaa tct ctg aaa aaa tat agt gac aaa tca 192
 Asn Ile Lys Gln Ala Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser
 50 55 60
 gca gaa aag agt cct ttt cca gaa gag aaa agt cac att ata gac aaa 240
 Ala Glu Lys Ser Pro Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys
 65 70 75 80

gaa gaa gat ata ggt aaa cgc agt ctt ttt cat tac aca agt tct ata	288
Glu Glu Asp Ile Gly Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile	
85 90 95	
acc aca aaa ttt gga gac tca ttc tac ttt tta tca aat cat att aat	336
Thr Thr Lys Phe Gly Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn	
100 105 110	
tca tat ttc aaa cgt aag gaa aaa atg tct caa caa aag gaa aat gaa	384
Ser Tyr Phe Lys Arg Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu	
115 120 125	
cat ttc cgg gac aaa tca gaa ctt gaa gat aaa aag gta gaa gag ggg	432
His Phe Arg Asp Lys Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly	
130 135 140	
aaa tta aga tct cca gat cct ggc atc ctg gct tat aag cca ggc tca	480
Lys Leu Arg Ser Pro Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser	
145 150 155 160	
gaa tct gta cat acg gtg gac aag cct aca agt cct tct gcg ata cct	528
Glu Ser Val His Thr Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro	
165 170 175	
gat gtt ctt caa gtt tca act aaa caa agt att gct aac ttt ctt tct	576
Asp Val Leu Gln Val Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser	
180 185 190	
cgt ccc acg gaa ggt gta caa gct tta gta ggt ggt tat att ggt gga	624
Arg Pro Thr Glu Gly Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly	
195 200 205	
ctt gtc ccc aaa tta aag tat gat tca aag agt cag tca gaa gaa cag	672
Leu Val Pro Lys Leu Lys Tyr Asp Ser Lys Ser Gln Ser Glu Glu Gln	
210 215 220	
gaa gag cct gct aaa act gat cag gct gtc agc aaa gac aga aat gca	720
Glu Glu Pro Ala Lys Thr Asp Gln Ala Val Ser Lys Asp Arg Asn Ala	
225 230 235 240	
gag gag aaa aag cgt tta tct ctt cag cga gaa aag att atc gca agg	768
Glu Glu Lys Lys Arg Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg	
245 250 255	
gtg agt att gat aac agg acc cgg gca tta gtt cag gca tta aga aga	816
Val Ser Ile Asp Asn Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg	
260 265 270	
aca act gac cca aag ctc tgc att act agg gtt gaa gaa ctg act ttt	864
Thr Thr Asp Pro Lys Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe	
275 280 285	
cat ctt cta gaa ttt cct gaa gga aaa gga gtg gct gtc aag gaa aga	912
His Leu Leu Glu Phe Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg	
290 295 300	

att att cca tat tta tta cga ctg aga caa att aag gat gaa act ctt	960
Ile Ile Pro Tyr Leu Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu	
305 310 315 320	
cag gct gca gtt aga gaa att ttg gcc cta att ggc tat gtg gat cca	1008
Gln Ala Ala Val Arg Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro	
325 330 335	
gtg aaa ggg aga gga atc cga att ctc tca att gat ggt gga gga aca	1056
Val Lys Gly Arg Gly Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr	
340 345 350	
agg ggc gtg gtt gct ctc cag acc cta cga aaa tta gtt gaa ctt act	1104
Arg Gly Val Val Ala Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr	
355 360 365	
cag aag cca gtt cat cag ctc ttt gat tac att tgt ggt gta agc aca	1152
Gln Lys Pro Val His Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr	
370 375 380	
ggg gcc ata tta gct ttc atg ttg ggg ttg ttt cat atg ccc ttg gat	1200
Gly Ala Ile Leu Ala Phe Met Leu Gly Leu Phe His Met Pro Leu Asp	
385 390 395 400	
gaa tgt gag gaa ctt tat cga aaa tta gga tca gat gta ttt tca caa	1248
Glu Cys Glu Glu Leu Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln	
405 410 415	
aat gtc att gtt gga aca gta aaa atg agt tgg agc cat gca ttt tat	1296
Asn Val Ile Val Gly Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr	
420 425 430	
gac agt caa aca tgg gaa aac att ctt aag gat agg atg gga tct gca	1344
Asp Ser Gln Thr Trp Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala	
435 440 445	
ctg atg att gaa aca gca aga aac ccc aca tgt cct aag gta gct gct	1392
Leu Met Ile Glu Thr Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala	
450 455 460	
gta agt acc ata gta aat aga ggg ata aca ccc aaa gct ttt gtg ttc	1440
Val Ser Thr Ile Val Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe	
465 470 475 480	
aga aac tat ggt cat ttt cct gga atc aac tct cat tat ttg gga ggc	1488
Arg Asn Tyr Gly His Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly	
485 490 495	
tgt cag tat aaa atg tgg cag gcc att aga gcc tca tct gct gct cca	1536
Cys Gln Tyr Lys Met Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro	
500 505 510	
ggc tac ttt gca gaa tat gca ttg gga aat gat ctt cat caa gat gga	1584
Gly Tyr Phe Ala Glu Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly	
515 520 525	

ggt ttg ctt ctg aat aac cct tcg gca tta gct atg cat gag tgt aaa	1632
Gly Leu Leu Leu Asn Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys	
530 535 540	
tgt ctt tgg cca gat gtg ccg tta gag tgc ata gta tcc ctg ggc act	1680
Cys Leu Trp Pro Asp Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr	
545 550 555 560	
gga cgt tat gag agt gat gtg aga aac acg gta aca tac aca agc ttg	1728
Gly Arg Tyr Glu Ser Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu	
565 570 575	
aaa act aaa ctt tct aat gtt atc aac agt gct aca gat aca gaa gaa	1776
Lys Thr Lys Leu Ser Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu	
580 585 590	
gtc cat ata atg ctt gat ggc ctg tta cct cct gac acc tat ttt aga	1824
Val His Ile Met Leu Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg	
595 600 605	
ttc aat cct gta atg tgt gaa aac ata cct cta gat gaa agt cga aat	1872
Phe Asn Pro Val Met Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn	
610 615 620	
gaa aag ctg gat cag ctg cag ttg gaa ggg ttg aaa tac ata gaa aga	1920
Glu Lys Leu Asp Gln Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg	
625 630 635 640	
aat gaa caa aaa atg aaa aaa gtt gca aaa ata tta agt caa gaa aaa	1968
Asn Glu Gln Lys Met Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys	
645 650 655	
aca act ctg cag aaa att aat gat tgg ata aaa tta aaa act gat atg	2016
Thr Thr Leu Gln Lys Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met	
660 665 670	
tat gaa gga ctt cca ttc ttt tca aaa ttg tga	2049
Tyr Glu Gly Leu Pro Phe Phe Ser Lys Leu	
675 680	

<210> 15

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 15

tgaacgtcga catgtcccgt attaaaa

27

<210> 16

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 16

gcatagcatg ctcacaattt tgaaaagaat ggaagtcc

38

<210> 17

<211> 661

<212> PRT

<213> Homo sapiens

<400> 17

Met	Ile	Ser	Arg	Leu	Ala	Gln	Phe	Lys	Pro	Ser	Ser	Gln	Ile	Leu	Arg
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Lys	Val	Ser	Asp	Ser	Gly	Trp	Leu	Lys	Gln	Lys	Asn	Ile	Lys	Gln	Ala
			20					25					30		

Ile	Lys	Ser	Leu	Lys	Lys	Tyr	Ser	Asp	Lys	Ser	Ala	Glu	Lys	Ser	Pro
		35					40					45			

Phe	Pro	Glu	Glu	Lys	Ser	His	Ile	Ile	Asp	Lys	Glu	Glu	Asp	Ile	Gly
	50					55					60				

Lys	Arg	Ser	Leu	Phe	His	Tyr	Thr	Ser	Ser	Ile	Thr	Thr	Lys	Phe	Gly
65					70					75					80

Asp	Ser	Phe	Tyr	Phe	Leu	Ser	Asn	His	Ile	Asn	Ser	Tyr	Phe	Lys	Arg
				85					90					95	

Lys	Glu	Lys	Met	Ser	Gln	Gln	Lys	Glu	Asn	Glu	His	Phe	Arg	Asp	Lys
			100					105					110		

Ser	Glu	Leu	Glu	Asp	Lys	Lys	Val	Glu	Glu	Gly	Lys	Leu	Arg	Ser	Pro
		115					120					125			

Asp	Pro	Gly	Ile	Leu	Ala	Tyr	Lys	Pro	Gly	Ser	Glu	Ser	Val	His	Thr
	130					135					140				

Val	Asp	Lys	Pro	Thr	Ser	Pro	Ser	Ala	Ile	Pro	Asp	Val	Leu	Gln	Val
145					150					155					160

Ser	Thr	Lys	Gln	Ser	Ile	Ala	Asn	Phe	Leu	Ser	Arg	Pro	Thr	Glu	Gly
			165						170					175	

Val	Gln	Ala	Leu	Val	Gly	Gly	Tyr	Ile	Gly	Gly	Leu	Val	Pro	Lys	Leu
			180					185					190		

Lys	Tyr	Asp	Ser	Lys	Ser	Gln	Ser	Glu	Glu	Gln	Glu	Glu	Pro	Ala	Lys
		195					200					205			

Thr	Asp	Gln	Ala	Val	Ser	Lys	Asp	Arg	Asn	Ala	Glu	Glu	Lys	Lys	Arg
	210					215					220				

Leu	Ser	Leu	Gln	Arg	Glu	Lys	Ile	Ile	Ala	Arg	Val	Ser	Ile	Asp	Asn
225					230					235					240

Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys
 245 250 255
 Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe
 260 265 270
 Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu
 275 280 285
 Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg
 290 295 300
 Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly
 305 310 315 320
 Ile Arg Ile Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala
 325 330 335
 Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His
 340 345 350
 Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala
 355 360 365
 Phe Met Leu Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu
 370 375 380
 Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly
 385 390 395 400
 Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp
 405 410 415
 Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr
 420 425 430
 Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val
 435 440 445
 Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His
 450 455 460
 Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met
 465 470 475 480
 Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu
 485 490 495
 Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn
 500 505 510
 Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp
 515 520 525
 Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser
 530 535 540

Asp Val Arg Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser
 545 550 555 560
 Asn Val Ile Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu
 565 570 575
 Asp Gly Leu Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met
 580 585 590
 Cys Glu Asn Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln
 595 600 605
 Leu Gln Leu Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met
 610 615 620
 Lys Lys Val Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys
 625 630 635 640
 Ile Asn Asp Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro
 645 650 655
 Phe Phe Ser Lys Leu
 660

<210> 18
 <211> 1986
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1986)

<400> 18
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 Met Ile Ser Arg Leu Ala Gln Phe Lys Pro Ser Ser Gln Ile Leu Arg
 1 5 10 15
 aaa gta tcg gat agt ggc tgg tta aaa cag aaa aac atc aaa caa gcc 96
 Lys Val Ser Asp Ser Gly Trp Leu Lys Gln Lys Asn Ile Lys Gln Ala
 20 25 30
 atc aaa tct ctg aaa aaa tat agt gac aaa tca gca gaa aag agt cct 144
 Ile Lys Ser Leu Lys Lys Tyr Ser Asp Lys Ser Ala Glu Lys Ser Pro
 35 40 45
 ttt cca gaa gag aaa agt cac att ata gac aaa gaa gaa gat ata ggt 192
 Phe Pro Glu Glu Lys Ser His Ile Ile Asp Lys Glu Glu Asp Ile Gly
 50 55 60
 aaa cgc agt ctt ttt cat tac aca agt tct ata acc aca aaa ttt gga 240
 Lys Arg Ser Leu Phe His Tyr Thr Ser Ser Ile Thr Thr Lys Phe Gly
 65 70 75 80
 gac tca ttc tac ttt tta tca aat cat att aat tca tat ttc aaa cgt 288
 Asp Ser Phe Tyr Phe Leu Ser Asn His Ile Asn Ser Tyr Phe Lys Arg
 85 90 95

aag gaa aaa atg tct caa caa aag gaa aat gaa cat ttc cgg gac aaa	336
Lys Glu Lys Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys	
100 105 110	
tca gaa ctt gaa gat aaa aag gta gaa gag ggg aaa tta aga tct cca	384
Ser Glu Leu Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro	
115 120 125	
gat cct ggc atc ctg gct tat aag cca ggc tca gaa tct gta cat acg	432
Asp Pro Gly Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr	
130 135 140	
gtg gac aag cct aca agt cct tct gcg ata cct gat gtt ctt caa gtt	480
Val Asp Lys Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val	
145 150 155 160	
tca act aaa caa agt att gct aac ttt ctt tct cgt ccc acg gaa ggt	528
Ser Thr Lys Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly	
165 170 175	
gta caa gct tta gta ggt ggt tat att ggt gga ctt gtc ccc aaa tta	576
Val Gln Ala Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu	
180 185 190	
aag tat gat tca aag agt cag tca gaa gaa cag gaa gag cct gct aaa	624
Lys Tyr Asp Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys	
195 200 205	
act gat cag gct gtc agc aaa gac aga aat gca gag gag aaa aag cgt	672
Thr Asp Gln Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg	
210 215 220	
tta tct ctt cag cga gaa aag att atc gca agg gtg agt att gat aac	720
Leu Ser Leu Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn	
225 230 235 240	
agg acc cgg gca tta gtt cag gca tta aga aga aca act gac cca aag	768
Arg Thr Arg Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys	
245 250 255	
ctc tgc att act agg gtt gaa gaa ctg act ttt cat ctt cta gaa ttt	816
Leu Cys Ile Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe	
260 265 270	
cct gaa gga aaa gga gtg gct gtc aag gaa aga att att cca tat tta	864
Pro Glu Gly Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu	
275 280 285	
tta cga ctg aga caa att aag gat gaa act ctt cag gct gca gtt aga	912
Leu Arg Leu Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg	
290 295 300	
gaa att ttg gcc cta att ggc tat gtg gat cca gtg aaa ggg aga gga	960
Glu Ile Leu Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly	
305 310 315 320	

atc cga att ctc tca att gat ggt gga gga aca agg ggc gtg gtt gct	1008
Ile Arg Ile Leu Ser Ile Asp Gly Gly Thr Arg Gly Val Val Ala	
325 330 335	
ctc cag acc cta cga aaa tta gtt gaa ctt act cag aag cca gtt cat	1056
Leu Gln Thr Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His	
340 345 350	
cag ctc ttt gat tac att tgt ggt gta agc aca ggt gcc ata tta gct	1104
Gln Leu Phe Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala	
355 360 365	
ttc atg ttg ggg ttg ttt cat atg ccc ttg gat gaa tgt gag gaa ctt	1152
Phe Met Leu Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu	
370 375 380	
tat cga aaa tta gga tca gat gta ttt tca caa aat gtc att gtt gga	1200
Tyr Arg Lys Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly	
385 390 395 400	
aca gta aaa atg agt tgg agc cat gca ttt tat gac agt caa aca tgg	1248
Thr Val Lys Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp	
405 410 415	
gaa aac att ctt aag gat agg atg gga tct gca ctg atg att gaa aca	1296
Glu Asn Ile Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr	
420 425 430	
gca aga aac ccc aca tgt cct aag gta gct gct gta agt acc ata gta	1344
Ala Arg Asn Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val	
435 440 445	
aat aga ggg ata aca ccc aaa gct ttt gtg ttc aga aac tat ggt cat	1392
Asn Arg Gly Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His	
450 455 460	
ttt cct gga atc aac tct cat tat ttg gga ggc tgt cag tat aaa atg	1440
Phe Pro Gly Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met	
465 470 475 480	
tgg cag gcc att aga gcc tca tct gct gct cca ggc tac ttt gca gaa	1488
Trp Gln Ala Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu	
485 490 495	
tat gca ttg gga aat gat ctt cat caa gat gga ggt ttg ctt ctg aat	1536
Tyr Ala Leu Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn	
500 505 510	
aac cct tcg gca tta gct atg cat gag tgt aaa tgt ctt tgg cca gat	1584
Asn Pro Ser Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp	
515 520 525	
gtg ccg tta gag tgc ata gta tcc ctg ggc act gga cgt tat gag agt	1632
Val Pro Leu Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser	
530 535 540	

gat	gtg	aga	aac	acg	gta	aca	tac	aca	agc	ttg	aaa	act	aaa	ctt	tct	1680
Asp	Val	Arg	Asn	Thr	Val	Thr	Tyr	Thr	Ser	Leu	Lys	Thr	Lys	Leu	Ser	
545					550				555						560	
aat	gtt	atc	aac	agt	gct	aca	gat	aca	gaa	gaa	gtc	cat	ata	atg	ctt	1728
Asn	Val	Ile	Asn	Ser	Ala	Thr	Asp	Thr	Glu	Glu	Val	His	Ile	Met	Leu	
			565						570					575		
gat	ggc	ctg	tta	cct	cct	gac	acc	tat	ttt	aga	ttc	aat	cct	gta	atg	1776
Asp	Gly	Leu	Leu	Pro	Pro	Asp	Thr	Tyr	Phe	Arg	Phe	Asn	Pro	Val	Met	
		580						585					590			
tgt	gaa	aac	ata	cct	cta	gat	gaa	agt	cga	aat	gaa	aag	ctg	gat	cag	1824
Cys	Glu	Asn	Ile	Pro	Leu	Asp	Glu	Ser	Arg	Asn	Glu	Lys	Leu	Asp	Gln	
		595				600						605				
ctg	cag	ttg	gaa	ggg	ttg	aaa	tac	ata	gaa	aga	aat	gaa	caa	aaa	atg	1872
Leu	Gln	Leu	Glu	Gly	Leu	Lys	Tyr	Ile	Glu	Arg	Asn	Glu	Gln	Lys	Met	
610					615						620					
aaa	aaa	gtt	gca	aaa	ata	tta	agt	caa	gaa	aaa	aca	act	ctg	cag	aaa	1920
Lys	Lys	Val	Ala	Lys	Ile	Leu	Ser	Gln	Glu	Lys	Thr	Thr	Leu	Gln	Lys	
625				630					635						640	
att	aat	gat	tgg	ata	aaa	tta	aaa	act	gat	atg	tat	gaa	gga	ctt	cca	1968
Ile	Asn	Asp	Trp	Ile	Lys	Leu	Lys	Thr	Asp	Met	Tyr	Glu	Gly	Leu	Pro	
			645					650						655		
ttc	ttt	tca	aaa	ttg	tga											1986
Phe	Phe	Ser	Lys	Leu												
			660													

<210> 19

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 19

tcaagtcgac atgatttcac gtttagc

27

<210> 20

<211> 38

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Primer

<400> 20

gcatagcatg ctcacaattt tgaaaagaat ggaagtcc

38

<210> 21
 <211> 562
 <212> PRT
 <213> Homo sapiens

<400> 21
 Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu
 1 5 10 15
 Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly
 20 25 30
 Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys
 35 40 45
 Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys
 50 55 60
 Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala
 65 70 75 80
 Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp
 85 90 95
 Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln
 100 105 110
 Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu
 115 120 125
 Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg
 130 135 140
 Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile
 145 150 155 160
 Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly
 165 170 175
 Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu
 180 185 190
 Arg Gln Ile Lys Asp Glu Thr Leu Gln Ala Ala Val Arg Glu Ile Leu
 195 200 205
 Ala Leu Ile Gly Tyr Val Asp Pro Val Lys Gly Arg Gly Ile Arg Ile
 210 215 220
 Leu Ser Ile Asp Gly Gly Gly Thr Arg Gly Val Val Ala Leu Gln Thr
 225 230 235 240
 Leu Arg Lys Leu Val Glu Leu Thr Gln Lys Pro Val His Gln Leu Phe
 245 250 255
 Asp Tyr Ile Cys Gly Val Ser Thr Gly Ala Ile Leu Ala Phe Met Leu
 260 265 270

Gly Leu Phe His Met Pro Leu Asp Glu Cys Glu Glu Leu Tyr Arg Lys
 275 280 285
 Leu Gly Ser Asp Val Phe Ser Gln Asn Val Ile Val Gly Thr Val Lys
 290 295 300
 Met Ser Trp Ser His Ala Phe Tyr Asp Ser Gln Thr Trp Glu Asn Ile
 305 310 315 320
 Leu Lys Asp Arg Met Gly Ser Ala Leu Met Ile Glu Thr Ala Arg Asn
 325 330 335
 Pro Thr Cys Pro Lys Val Ala Ala Val Ser Thr Ile Val Asn Arg Gly
 340 345 350
 Ile Thr Pro Lys Ala Phe Val Phe Arg Asn Tyr Gly His Phe Pro Gly
 355 360 365
 Ile Asn Ser His Tyr Leu Gly Gly Cys Gln Tyr Lys Met Trp Gln Ala
 370 375 380
 Ile Arg Ala Ser Ser Ala Ala Pro Gly Tyr Phe Ala Glu Tyr Ala Leu
 385 390 395 400
 Gly Asn Asp Leu His Gln Asp Gly Gly Leu Leu Leu Asn Asn Pro Ser
 405 410 415
 Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu
 420 425 430
 Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg
 435 440 445
 Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile
 450 455 460
 Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu
 465 470 475 480
 Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn
 485 490 495
 Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu
 500 505 510
 Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val
 515 520 525
 Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp
 530 535 540
 Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe Ser
 545 550 555 560
 Lys Leu

<210> 22
 <211> 1689
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(1689)

<400> 22
 atg tct caa caa aag gaa aat gaa cat ttc cgg gac aaa tca gaa ctt 48
 Met Ser Gln Gln Lys Glu Asn Glu His Phe Arg Asp Lys Ser Glu Leu
 1 5 10 15

gaa gat aaa aag gta gaa gag ggg aaa tta aga tct cca gat cct ggc 96
 Glu Asp Lys Lys Val Glu Glu Gly Lys Leu Arg Ser Pro Asp Pro Gly
 20 25 30

atc ctg gct tat aag cca ggc tca gaa tct gta cat acg gtg gac aag 144
 Ile Leu Ala Tyr Lys Pro Gly Ser Glu Ser Val His Thr Val Asp Lys
 35 40 45

cct aca agt cct tct gcg ata cct gat gtt ctt caa gtt tca act aaa 192
 Pro Thr Ser Pro Ser Ala Ile Pro Asp Val Leu Gln Val Ser Thr Lys
 50 55 60

caa agt att gct aac ttt ctt tct cgt ccc acg gaa ggt gta caa gct 240
 Gln Ser Ile Ala Asn Phe Leu Ser Arg Pro Thr Glu Gly Val Gln Ala
 65 70 75 80

tta gta ggt ggt tat att ggt gga ctt gtc ccc aaa tta aag tat gat 288
 Leu Val Gly Gly Tyr Ile Gly Gly Leu Val Pro Lys Leu Lys Tyr Asp
 85 90 95

tca aag agt cag tca gaa gaa cag gaa gag cct gct aaa act gat cag 336
 Ser Lys Ser Gln Ser Glu Glu Gln Glu Glu Pro Ala Lys Thr Asp Gln
 100 105 110

gct gtc agc aaa gac aga aat gca gag gag aaa aag cgt tta tct ctt 384
 Ala Val Ser Lys Asp Arg Asn Ala Glu Glu Lys Lys Arg Leu Ser Leu
 115 120 125

cag cga gaa aag att atc gca agg gtg agt att gat aac agg acc cgg 432
 Gln Arg Glu Lys Ile Ile Ala Arg Val Ser Ile Asp Asn Arg Thr Arg
 130 135 140

gca tta gtt cag gca tta aga aga aca act gac cca aag ctc tgc att 480
 Ala Leu Val Gln Ala Leu Arg Arg Thr Thr Asp Pro Lys Leu Cys Ile
 145 150 155 160

act agg gtt gaa gaa ctg act ttt cat ctt cta gaa ttt cct gaa gga 528
 Thr Arg Val Glu Glu Leu Thr Phe His Leu Leu Glu Phe Pro Glu Gly
 165 170 175

aaa gga gtg gct gtc aag gaa aga att att cca tat tta tta cga ctg 576
 Lys Gly Val Ala Val Lys Glu Arg Ile Ile Pro Tyr Leu Leu Arg Leu
 180 185 190

aga	caa	att	aag	gat	gaa	act	ctt	cag	gct	gca	gtt	aga	gaa	att	ttg	624
Arg	Gln	Ile	Lys	Asp	Glu	Thr	Leu	Gln	Ala	Ala	Val	Arg	Glu	Ile	Leu	
		195					200					205				
gcc	cta	att	ggc	tat	gtg	gat	cca	gtg	aaa	ggg	aga	gga	atc	cga	att	672
Ala	Leu	Ile	Gly	Tyr	Val	Asp	Pro	Val	Lys	Gly	Arg	Gly	Ile	Arg	Ile	
	210					215					220					
ctc	tca	att	gat	ggg	gga	gga	aca	agg	ggc	gtg	gtt	gct	ctc	cag	acc	720
Leu	Ser	Ile	Asp	Gly	Gly	Gly	Thr	Arg	Gly	Val	Val	Ala	Leu	Gln	Thr	
225					230					235					240	
cta	cga	aaa	tta	gtt	gaa	ctt	act	cag	aag	cca	gtt	cat	cag	ctc	ttt	768
Leu	Arg	Lys	Leu	Val	Glu	Leu	Thr	Gln	Lys	Pro	Val	His	Gln	Leu	Phe	
			245						250					255		
gat	tac	att	tgt	ggg	gta	agc	aca	ggg	gcc	ata	tta	gct	ttc	atg	ttg	816
Asp	Tyr	Ile	Cys	Gly	Val	Ser	Thr	Gly	Ala	Ile	Leu	Ala	Phe	Met	Leu	
		260						265					270			
ggg	ttg	ttt	cat	atg	ccc	ttg	gat	gaa	tgt	gag	gaa	ctt	tat	cga	aaa	864
Gly	Leu	Phe	His	Met	Pro	Leu	Asp	Glu	Cys	Glu	Glu	Leu	Tyr	Arg	Lys	
		275					280					285				
tta	gga	tca	gat	gta	ttt	tca	caa	aat	gtc	att	gtt	gga	aca	gta	aaa	912
Leu	Gly	Ser	Asp	Val	Phe	Ser	Gln	Asn	Val	Ile	Val	Gly	Thr	Val	Lys	
	290					295					300					
atg	agt	tggt	agc	cat	gca	ttt	tat	gac	agt	caa	aca	tggt	gaa	aac	att	960
Met	Ser	Trp	Ser	His	Ala	Phe	Tyr	Asp	Ser	Gln	Thr	Trp	Glu	Asn	Ile	
305					310					315					320	
ctt	aag	gat	agg	atg	gga	tct	gca	ctg	atg	att	gaa	aca	gca	aga	aac	1008
Leu	Lys	Asp	Arg	Met	Gly	Ser	Ala	Leu	Met	Ile	Glu	Thr	Ala	Arg	Asn	
				325					330					335		
ccc	aca	tgt	cct	aag	gta	gct	gct	gta	agt	acc	ata	gta	aat	aga	ggg	1056
Pro	Thr	Cys	Pro	Lys	Val	Ala	Ala	Val	Ser	Thr	Ile	Val	Asn	Arg	Gly	
			340					345					350			
ata	aca	ccc	aaa	gct	ttt	gtg	ttc	aga	aac	tat	ggg	cat	ttt	cct	gga	1104
Ile	Thr	Pro	Lys	Ala	Phe	Val	Phe	Arg	Asn	Tyr	Gly	His	Phe	Pro	Gly	
		355				360						365				
atc	aac	tct	cat	tat	ttg	gga	ggc	tgt	cag	tat	aaa	atg	tggt	cag	gcc	1152
Ile	Asn	Ser	His	Tyr	Leu	Gly	Gly	Cys	Gln	Tyr	Lys	Met	Trp	Gln	Ala	
	370					375					380					
att	aga	gcc	tca	tct	gct	gct	cca	ggc	tac	ttt	gca	gaa	tat	gca	ttg	1200
Ile	Arg	Ala	Ser	Ser	Ala	Ala	Pro	Gly	Tyr	Phe	Ala	Glu	Tyr	Ala	Leu	
	385				390				395						400	
gga	aat	gat	ctt	cat	caa	gat	gga	ggg	ttg	ctt	ctg	aat	aac	cct	tcg	1248
Gly	Asn	Asp	Leu	His	Gln	Asp	Gly	Gly	Leu	Leu	Leu	Asn	Asn	Pro	Ser	
				405					410					415		

gca tta gct atg cat gag tgt aaa tgt ctt tgg cca gat gtg ccg tta	1296
Ala Leu Ala Met His Glu Cys Lys Cys Leu Trp Pro Asp Val Pro Leu	
420 425 430	
gag tgc ata gta tcc ctg ggc act gga cgt tat gag agt gat gtg aga	1344
Glu Cys Ile Val Ser Leu Gly Thr Gly Arg Tyr Glu Ser Asp Val Arg	
435 440 445	
aac acg gta aca tac aca agc ttg aaa act aaa ctt tct aat gtt atc	1392
Asn Thr Val Thr Tyr Thr Ser Leu Lys Thr Lys Leu Ser Asn Val Ile	
450 455 460	
aac agt gct aca gat aca gaa gaa gtc cat ata atg ctt gat ggc ctg	1440
Asn Ser Ala Thr Asp Thr Glu Glu Val His Ile Met Leu Asp Gly Leu	
465 470 475 480	
tta cct cct gac acc tat ttt aga ttc aat cct gta atg tgt gaa aac	1488
Leu Pro Pro Asp Thr Tyr Phe Arg Phe Asn Pro Val Met Cys Glu Asn	
485 490 495	
ata cct cta gat gaa agt cga aat gaa aag ctg gat cag ctg cag ttg	1536
Ile Pro Leu Asp Glu Ser Arg Asn Glu Lys Leu Asp Gln Leu Gln Leu	
500 505 510	
gaa ggg ttg aaa tac ata gaa aga aat gaa caa aaa atg aaa aaa gtt	1584
Glu Gly Leu Lys Tyr Ile Glu Arg Asn Glu Gln Lys Met Lys Lys Val	
515 520 525	
gca aaa ata tta agt caa gaa aaa aca act ctg cag aaa att aat gat	1632
Ala Lys Ile Leu Ser Gln Glu Lys Thr Thr Leu Gln Lys Ile Asn Asp	
530 535 540	
tgg ata aaa tta aaa act gat atg tat gaa gga ctt cca ttc ttt tca	1680
Trp Ile Lys Leu Lys Thr Asp Met Tyr Glu Gly Leu Pro Phe Phe Ser	
545 550 555 560	
aaa ttg tga	1689
Lys Leu	

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27

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cattcctctc cctttcactg gatccacata gcc

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 1 5 10 15

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 consensus motif

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 oligonucleotide

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 oligonucleotide

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 oligonucleotide

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1 5

27

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1 5

a1
cont